GenCore version 5.1.5

OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 16:20:34 ; Search time 247.669 Seconds
(without alignments)
10774.128 Million cell updates/sec

Title: US-09-625-573-3
Perfect score: 1979
Sequence: 1 CAGGACTGCCTGAGACAAGC.....ATATGCAATATAAAATTTAG 1979

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1943.8	98.2	143068	10	US-09-967-768A-316	Sequence 316, App
2	1081.4	54.6	1083	10	US-09-131-827A-1	Sequence 1, Appli
3	1079.8	54.6	1083	10	US-09-131-827A-19	Sequence 19, Appl
4	704.6	35.6	1059	12	US-10-106-623-19	Sequence 19, Appl
5	703.4	35.5	1225	10	US-09-813-653-14	Sequence 14, Appl
6	703.4	35.5	1376	9	US-10-086-814-2	Sequence 2, Appli
7	703.4	35.5	1376	10	US-09-796-202-2	Sequence 2, Appli
8	703.4	35.5	1477	10	US-09-759-841-1	Sequence 1, Appli
9	703.4	35.5	1477	10	US-09-938-719-2	Sequence 2, Appli
10	703.4	35.5	1477	10	US-09-939-226-2	Sequence 2, Appli
11	703.4	35.5	1477	10	US-09-938-703-2	Sequence 2, Appli
12	703.4	35.5	3383	9	US-09-734-221A-13	Sequence 13, Appl
13	703.4	35.5	3383	12	US-10-106-623-1	Sequence 1, Appli
14	701.8	35.5	1225	10	US-09-813-653-16	Sequence 16, Appl
15	701.8	35.5	1414	9	US-10-232-686-1	Sequence 1, Appli
16	701.8	35.5	1414	10	US-09-725-285-1	Sequence 1, Appli
17	701.8	35.5	1414	10	US-09-195-662A-1	Sequence 1, Appli
18	701.8	35.5	1414	10	US-09-339-912A-1	Sequence 1, Appli
19	701.8	35.5	1414	10	US-09-502-783A-1	Sequence 1, Appli
20	700.2	35.4	1414	10	US-09-779-879A-1	Sequence 1, Appli
21	700.2	35.4	1414	10	US-09-779-880A-1	Sequence 1, Appli
22	697.6	35.3	1056	10	US-09-779-879A-21	Sequence 21, Appl
23	697.6	35.3	1056	10	US-09-779-880A-21	Sequence 21, Appl
24	683.4	34.5	1442	10	US-09-938-719-3	Sequence 3, Appli
25	683.4	34.5	1442	10	US-09-939-226-3	Sequence 3, Appli
26	683.4	34.5	1442	10	US-09-938-703-3	Sequence 3, Appli
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30	350.2	17.7	1689	10	US-09-931-381A-15	Sequence 15, Appl
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34	341	17.2	3426	9	US-10-001-835-29	Sequence 29, Appl
35	304	15.4	1607	9	US-10-120-394-19	Sequence 19, Appl
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37	299	15.1	1677	10	US-09-837-446-1	Sequence 1, Appli
38	277.2	14.0	1318	10	US-09-917-800A-1445	Sequence 1445, Ap
39	268.4	13.6	1487	10	US-09-789-482-3	Sequence 3, Appli
40	268.4	13.6	1487	10	US-09-789-486-3	Sequence 3, Appli
41	266.8	13.5	3100	10	US-09-954-456-267	Sequence 267, App
42	266.8	13.5	3100	10	US-09-954-456-945	Sequence 945, App
43	266.8	13.5	3100	10	US-09-954-456-1588	Sequence 1588, Ap
44	261.2	13.2	1586	10	US-09-104-792-1	Sequence 1, Appli
45	181.6	9.2	1050	10	US-09-912-025-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-967-768A-316
; Sequence 316, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Si
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 316
; LENGTH: 143068
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-316

Query Match 98.2%; Score 1943.8; DB 10; Length 143068;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1945; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy     207 CAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTG 266
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Qy   1887 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 1946
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Db  47912 CATCCCCCTGTCTAAAAATTCAGAAAATTTTTGTTTATAAAAGATGCATTATCTATGATA 47971

Qy   1947 TGCTAATATATGTATATGCAATATAAA 1973
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Db  47972 TGCTAATATATGTATATGCAATATATA 47998
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RESULT 2
US-09-131-827A-1
; Sequence 1, Application US/09131827A
; Patent No. US20020038469A1
; GENERAL INFORMATION:
;  APPLICANT:  Dean, Michael
;  APPLICANT:  O'Brien, Stephen J.
;  APPLICANT:  Smith, Michael
;  APPLICANT:  Carrington, Mary
;  TITLE OF INVENTION:  DELAYED PROGRESSION TO AIDS BY A
;  TITLE OF INVENTION:  MISSENSE ALLELE OF THE CCR2 GENE
;  FILE REFERENCE:  14014.0333
;  CURRENT APPLICATION NUMBER: US/09/131,827A
;  CURRENT FILING DATE:  1998-08-10
;  PRIOR APPLICATION NUMBER:  60/055,659
;  PRIOR FILING DATE:  1997-08-14
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1080)
US-09-131-827A-1
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  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1082;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy     141 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 200
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Db     361 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 420

Qy     501 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 560
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Db     421 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 480

Qy     561 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 620
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Db     481 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 540

Qy     621 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 680
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Qy    1041 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1100
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Qy    1161 TAA 1163
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Db    1081 TAA 1083
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RESULT 3
US-09-131-827A-19
; Sequence 19, Application US/09131827A
; Patent No. US20020038469A1
; GENERAL INFORMATION:
;  APPLICANT:  Dean, Michael
;  APPLICANT:  O'Brien, Stephen J.
;  APPLICANT:  Smith, Michael
;  APPLICANT:  Carrington, Mary
;  TITLE OF INVENTION:  DELAYED PROGRESSION TO AIDS BY A
;  TITLE OF INVENTION:  MISSENSE ALLELE OF THE CCR2 GENE
;  FILE REFERENCE:  14014.0333
;  CURRENT APPLICATION NUMBER: US/09/131,827A
;  CURRENT FILING DATE:  1998-08-10
;  PRIOR APPLICATION NUMBER:  60/055,659
;  PRIOR FILING DATE:  1997-08-14
;  NUMBER OF SEQ ID NOS:  20
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 1083
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-131-827A-19

  Query Match             54.6%;  Score 1079.8;  DB 10;  Length 1083;
  Best Local Similarity   99.8%;  Pred. No. 6.5e-315;
  Matches 1081;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      81 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGCTGTCCACATCTCGTTCTCGGTTTATCAGAAATACCAACGAGAGCGGTGAAGAAGTC 60

Qy     141 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACCACCTTTTTTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATT 120

Qy     201 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGGGCCCAACTCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAAC 180

Qy     261 ATGCTGGTCGTCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 320
           |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATGCTGGTCATCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTAC 240

Qy     321 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGCTCAACCTGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCAC 300

Qy     381 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCTGCTGCAAATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTAT 360

Qy     441 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTG 420

Qy     501 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GCTATTGTCCATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACA 480

Qy     561 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAA 540
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Qy     621 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TGCCAGAAAGAAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCACGAGGATGGAATAAT 600

Qy     681 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATC 660

Qy     741 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGG 720

Qy     801 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAC 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAAT 780

Qy     861 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACC 840

Qy     921 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATC 900

Qy     981 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 AATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTC 960

Qy    1041 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTG 1020

Qy    1101 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 GATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTA 1080

Qy    1161 TAA 1163
           |||
Db    1081 TAA 1083
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RESULT 4
US-10-106-623-19
; Sequence 19, Application US/10106623
; Patent No. US20020150888A1
;   GENERAL INFORMATION:
;        APPLICANT: Gray, Patrick W.
;                   Schweickart, Vicky L.
;                   Raport, Carol J.
;        TITLE OF INVENTION: Chemokine Receptor Materials and Methods
;        NUMBER OF SEQUENCES: 20
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;             STREET: 6300 Sears Tower, 233 S. Wacker Drive
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/106,623
;             FILING DATE: 26-Mar-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/771,276
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: No. US20020150888A1and, Greta E.
;             REGISTRATION NUMBER: 35,302
;             REFERENCE/DOCKET NUMBER: 27866/33670
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312-474-6300
;             TELEFAX: 312-474-0448
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1059 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1056
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-106-623-19

  Query Match           35.6%;  Score 704.6;  DB 12;  Length 1059;
  Best Local Similarity  81.4%;  Pred. No. 1.1e-201;
  Matches  834;  Conservative    0;  Mismatches  179;  Indels   12;  Gaps    1;
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Qy     151 TTGATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAAC 210
           | |||||| ||       |  ||||| || ||| |  | ||||| ||||| |  |||| |
Db      35 TCGATTATTATACATCGGAACCCTGCCAAAAAATCAATGTGAAACAAATCGCAGCCCGCC 94

Qy     211 TCCTGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCG 270
           |||||||||||||||||| ||||||||||||||||||||||||||||||| |||||||
Db      95 TCCTGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGGCAACATACTGGTCG 154

Qy     271 TCCTCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACC 330
           |||||||| | |||||||||||||| ||||||  || |||||||||| ||||||||||||
Db     155 TCCTCATCCTGATAAACTGCAAAAGGCTGAAAAGCATGACTGACATCTACCTGCTCAACC 214

Qy     331 TGGCCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAA 390
           |||||||||||||| |||||||| ||| ||||| |||| || ||||||||||| ||||||
Db     215 TGGCCATCTCTGACCTGCTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCTG 274

Qy     391 ATGAGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTT 450
           ||||||| |||||| ||| |||||||  || | || |||||||| |||   || || |
Db     275 CCCAGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCT 334

Qy     451 ATTTTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCC 510
           ||    |||||||||||||||||||||||||||||||||||| |||||||||| ||||
Db     335 TCTTCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTATCGTCC 394

Qy     511 ATGCTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCA 570
           |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     395 ATGCTGTGTTTGCTTTAAAAGCCAGGACAGTCACCTTTGGGGTGGTGACAAGTGTGATCA 454

Qy     571 CCTGGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAG 630
           | ||| |||||||||||||||| ||| |||||||||||||||||| | ||  |||| ||
Db     455 CTTGGGTGGTGGCTGTGTTTGCCTCTCTCCCAGGAATCATCTTTACCAGATCTCAGAGAG 514

Qy     631 AAGATTCTGTTTATGTCTGTGGCCCTTATTTTCCA-----------CGAGGATGGAATA 678
           ||| |  |  |||   |||  || || ||||||||           | |  ||||| |
Db     515 AAGGTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGA 574

Qy     679 ATTTCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCA 738
           |||| || ||| ||| || |  ||| ||||||||||||||||||||  |||||||||
Db     575 ATTTTCAGACATTAAAGATGGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCA 634

Qy     739 TCTGCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATA 798
           |||||||||||||||||||||| ||||||||||||||||||||||||||||||||| |
Db     635 TCTGCTACTCGGGAATCCTGAAAACTCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCACA 694

Qy     799 GGGCAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATA 858
           |||| |||||  | |||||||||||||||||||| |||||||| ||| ||||||| |
Db     695 GGGCTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTGTGGGCTCCCTACA 754

Qy     859 ACATTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCA 918
           |||||||| |||||||||||||||||||||||||||||| ||||||| ||| ||    |||
Db     755 ACATTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCT 814
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Qy    919 CCAGTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCA 978
          | |      |||||||||||| ||||||||||||||||||||||||||| ||||||||||
Db    815 CTAACAGGTTGGACCAAGCCATGCAGGTGACAGAGACTCTTGGGATGACACACTGCTGCA 874

Qy    979 TCAATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCT 1038
          |||| |||||||||||||||| || ||||||||||||||||  || ||||  || ||||
Db    875 TCAACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCT 934

Qy   1039 TCCGAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAG 1098
          ||| |||||||||  |||| ||||||||||||   ||| |  ||||| |    ||| |
Db    935 TCCAAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCCATTTTCCAGCAAGAGGCTC 994

Qy   1099 TGGATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTT 1158
            ||  |||  | ||||    |||| |  ||||||||||||||||| | || |  || |
Db    995 CCGAGCGAGCAAGTTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCT 1054

Qy   1159 TATAA 1163
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Db   1055 TGTGA 1059
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RESULT 5
US-09-813-653-14
; Sequence 14, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(1085)
US-09-813-653-14

Query Match 35.5%; Score 703.4; DB 10; Length 1225;
Best Local Similarity 80.5%; Pred. No. 2.8e-201;
Matches 840; Conservative 0; Mismatches 191; Indels 12; Gaps 1;

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Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213
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Db     64 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 123

Qy    214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCC 273
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||| |||
Db    124 TGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCC 183

Qy    274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333
          ||||| | |||||||||||| ||||||| || |||||||||| ||||||||||||||||
Db    184 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 243

Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG 393
          |||||||||| ||| |||| ||| ||||| |||| || ||||||||| ||||||
Db    244 CCATCTCTGACCTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCC 303

Qy    394 AGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATT 453
          |||||| |||||| ||| ||||||| || | || |||||||| |||   || || |  |
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Db    304 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT 363

Qy    454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
          |    |||||||||||||||||||||||||||||||||| ||||||||| | |||||||
Db    364 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 423

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    424 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 483

Qy    574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633
          || |||||||||||||| ||| |||||||||||||||||| | ||  || |||||||
Db    484 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 543

Qy    634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA-----------CGAGGATGGAATAATT 681
          |  |  |||   |||  || || ||||||||           | |   ||||| ||||
Db    544 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 603

Qy    682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741
          |||| ||| ||| ||    ||| ||||||||||||||||||||  ||||||||||||
Db    604 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCT 663

Qy    742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG 801
          |||||||||||||||| ||||| |||||||||||||||| |||||||||||||| ||||
Db    664 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 723

Qy    802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA 861
          | |||||  | ||||||||||||||||||||||| |||||||||| |||||| ||||
Db    724 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 783

Qy    862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921
          ||||| |||||||||||||||||||||||||||||| ||||||| ||| ||    ||| | |
Db    784 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA 843

Qy    922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA 981
                |||||||||| | ||||||||||||||||||||||||| ||||||||||||
Db    844 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 903

Qy    982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC 1041
          | |||||||||||||||| || ||||||||||||||  || ||||  || |||||||
Db    904 ACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 963

Qy   1042 GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 1101
            |||||||||  |||| ||||||||||||   ||| |  ||||| |    ||| |    |
Db    964 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCG 1023

Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTAT 1161
          |  |||  |  |||    |||| |  ||||||||||||||||| | || |  || || |
Db   1024 AGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT 1083

Qy   1162 AAAACGAGGAGCAGTTTGATTGT 1184
            | |||       |||  | | ||
Db   1084 GACACGGACTCAAGTGGGCTGGT 1106
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RESULT 6
US-10-086-814-2
; Sequence 2, Application US/10086814
; Publication No. US20030092632A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, Wlliam C.
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 61010-AB-1
; CURRENT APPLICATION NUMBER: US/10/086,814
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-086-814-2

Query Match 35.5%; Score 703.4; DB 9; Length 1376;
Best Local Similarity 80.5%; Pred. No. 3e-201;
Matches 840; Conservative 0; Mismatches 191; Indels 12; Gaps 1;

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Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213
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Db    277 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 336

Qy    214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCC 273
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||| |||
Db    337 TGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCC 396

Qy    274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333
          |||||  | |||||||||||||| ||||||| || |||||||||| ||||||||||||||||
Db    397 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 456

Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG 393
          ||||||||| ||| |||| ||| ||||| |||| || |||||||||| ||||||
Db    457 CCATCTCTGACCTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCC 516

Qy    394 AGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATT 453
          ||||||  |||||| ||| |||||||  || | || ||||||||  |||   || || |  |
Db    517 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT 576

Qy    454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
          |    ||||||||||||||||||||||||||||||||||||||||| |||||||| | |||||||
Db    577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 636

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    637 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 696

Qy    574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633
          ||  |||||||||||||||| ||| |||||||||||||||||| | ||  || |||||||
Db    697 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 756

Qy    634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA----------CGAGGATGGAATAATT 681
          |  |  |||   |||  || || ||||||||           | |   ||||| ||||
Db    757 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 816

Qy    682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741
          |||| ||| ||| ||    ||| ||||||||||||||||||||||  ||||||||||||
Db    817 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCT 876

Qy    742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG 801
          |||||||||||||||| ||||| |||||||||||||||| ||||||||||||| ||||
Db    877 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 936

Qy    802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA 861
          | |||||  | |||||||||||||||||||||||||||| |||||||||| ||||||| ||||
Db    937 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 996

Qy    862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921
          |||||  |||||||||||||||||||||||||||||||| ||||||| ||| ||    ||| | |
Db    997 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA 1056

Qy    922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA 981
          |||||||||| | |||||||||||||||||||||||||||| ||||||||||||
Db   1057 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 1116

Qy    982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC 1041
          | |||||||||||||||| || |||||||||||||||  || ||||  || ||||||||
Db   1117 ACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 1176

Qy   1042 GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 1101
          |||||||||  |||| ||||||||||||   ||| | |||||  |    ||| |    |
Db   1177 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCG 1236

Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTAT 1161
          |  |||  | |||    |||| |  |||||||||||||||||| | || |  || || |
Db   1237 AGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT 1296
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Qy    1162 AAAACGAGGAGCAGTTTGATTGT 1184
           | |||      |||  | | ||
Db    1297 GACACGGACTCAAGTGGGCTGGT 1319
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RESULT 7
US-09-796-202-2
; Sequence 2, Application US/09796202
; Patent No. US20020068813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPW/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: human
US-09-796-202-2

Query Match 35.5%; Score 703.4; DB 10; Length 1376;
Best Local Similarity 80.5%; Pred. No. 3e-201;
Matches 840; Conservative 0; Mismatches 191; Indels 12; Gaps 1;

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Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213
          ||||| ||      |  ||||| || ||| |  | ||||||||||| |  ||||  ||||
Db    277 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 336

Qy    214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCC 273
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||| |||
Db    337 TGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCC 396

Qy    274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333
          |||||  | |||||||||||||| ||||||| || |||||||||| ||||||||||||||||
Db    397 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 456

Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG 393
          ||||||||| ||| |||| ||| ||||| |||| || |||||||||| ||||||
Db    457 CCATCTCTGACCTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCC 516

Qy    394 AGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATT 453
          ||||||  |||||| ||| |||||||  || | || ||||||||  |||   || || |  |
Db    517 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT 576

Qy    454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
          |    ||||||||||||||||||||||||||||||||||||||||| |||||||| | |||||||
Db    577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 636

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    637 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 696

Qy    574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633
          ||  |||||||||||||||| ||| |||||||||||||||||| | ||  || |||||||
Db    697 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 756

Qy    634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA----------CGAGGATGGAATAATT 681
          |  |  |||   |||  || || ||||||||           | |   ||||| ||||
Db    757 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 816

Qy    682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741
          |||| ||| ||| ||    ||| ||||||||||||||||||||||  ||||||||||||
Db    817 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCT 876

Qy    742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG 801
          |||||||||||||||| ||||| |||||||||||||||| ||||||||||||| ||||
Db    877 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 936

Qy    802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA 861
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Db    937 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 996

Qy    862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921
          ||||| ||||||||||||||||||||||||||||| |||||| ||| ||    ||| | |
Db    997 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA 1056

Qy    922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA 981
          |||||||||| | ||||||||||||||||||||||||||||| ||||||||||||
Db   1057 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 1116

Qy    982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC 1041
          | ||||||||||||||||| || ||||||||||||||||  || ||||  || |||||||
Db   1117 ACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 1176

Qy   1042 GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 1101
          |||||||||  |||| ||||||||||||    ||| |  |||| |    ||| |    |
Db   1177 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCG 1236

Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTAT 1161
          |  |||  |  |||    |||| |  |||||||||||||||| | || |  || || |
Db   1237 AGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT 1296

Qy   1162 AAAACGAGGAGCAGTTTGATTGT 1184
           | |||      |||  | | ||
Db   1297 GACACGGACTCAAGTGGGCTGGT 1319
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RESULT 8
US-09-759-841-1
; Sequence 1, Application US/09759841
; Patent No. US20010039026A1
; GENERAL INFORMATION:
; APPLICANT: Rickett, Graham A
; APPLICANT: Dobbs, Susan
; APPLICANT: Perros, Manoussos
; TITLE OF INVENTION: Assay Method
; FILE REFERENCE: PC10348APME
; CURRENT APPLICATION NUMBER: US/09/759,841
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: GB 0000661.9
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000663.5
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: GB 0000659.3
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1477
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1377, 1384, 1385
; OTHER INFORMATION: n is a or g or c or t/u
US-09-759-841-1

Query Match 35.5%; Score 703.4; DB 10; Length 1477;
Best Local Similarity 80.5%; Pred. No. 3.1e-201;
Matches 840; Conservative 0; Mismatches 191; Indels 12; Gaps 1;

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Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213
          ||||| ||      | ||||| || ||| |  | ||||||||||| |  ||||  ||||
Db    277 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 336

Qy    214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCC 273
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||| |||
Db    337 TGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCC 396

Qy    274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333
          ||||| | |||||||||||| ||||||| || |||||||||| ||||||||||||||||
Db    397 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 456
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Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG 393
          |||||||||| ||| |||| ||| ||||| |||| || |||||||||| ||||||
Db    457 CCATCTCTGACCTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCC 516

Qy    394 AGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATT 453
          |||||| |||||| ||| |||||||  || | || |||||||| |||   || || |  |
Db    517 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT 576

Qy    454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
          |    |||||||||||||||||||||||||||||||||||||||||| ||||||||| | |||||||
Db    577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 636

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    637 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 696

Qy    574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633
          || |||||||||||||||| ||| |||||||||||||||||| | ||  || |||||||
Db    697 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 756

Qy    634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA----------CGAGGATGGAATAATT 681
          |  |  |||   |||  || || ||||||||           | |   ||||| ||||
Db    757 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 816

Qy    682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741
          |||| ||| ||| ||    ||| ||||||||||||||||||||||  ||||||||||||
Db    817 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCT 876

Qy    742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG 801
          |||||||||||||||| ||||| ||||||||||||||||| ||||||||||||| ||||
Db    877 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 936

Qy    802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA 861
          | |||||  | ||||||||||||||||||||||| |||||||||||| ||||||| ||||
Db    937 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 996

Qy    862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921
          ||||| ||||||||||||||||||||||||||||| |||||| ||| ||    ||| | |
Db    997 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA 1056

Qy    922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA 981
          |||||||||| | ||||||||||||||||||||||||||||| ||||||||||||
Db   1057 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 1116

Qy    982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC 1041
          | ||||||||||||||||| || ||||||||||||||||  || ||||  || |||||||
Db   1117 ACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 1176

Qy   1042 GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 1101
          |||||||||  |||| ||||||||||||    ||| |  |||| |    ||| |    |
Db   1177 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCG 1236

Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTAT 1161
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Db   1237 AGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT 1296

Qy   1162 AAAACGAGGAGCAGTTTGATTGT 1184
           | |||      |||  | | ||
Db   1297 GACACGGACTCAAGTGGGCTGGT 1319
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RESULT 9
US-09-938-719-2
; Sequence 2, Application US/09938719
; Patent No. US20020106742A1
; GENERAL INFORMATION:
; APPLICANT: SAMSON, MICHEL
; PARMENTIER, MARC
; VASSART, GILBERT
; LIBERT, FREDERICK
; TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
; AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

```
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive  16th Floor
;            CITY: Newport Beach
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/938,719
;            FILING DATE: 24-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/626,939
;            FILING DATE: 27-JULY-2000
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Altman, Daniel E
;            REGISTRATION NUMBER: 34,115
;            REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1477 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  240..1295
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-938-719-2

  Query Match             35.5%;  Score 703.4;  DB 10;  Length 1477;
  Best Local Similarity   80.5%;  Pred. No. 3.1e-201;
  Matches  840;  Conservative    0;  Mismatches  191;  Indels   12;  Gaps    1;

Qy     154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213
           ||||| ||      | ||||| || ||| |  | ||||||||||| | ||||  ||||
Db     277 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 336

Qy     214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCC 273
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||| |||
Db     337 TGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCC 396

Qy     274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333
           ||||| | |||||||||||| ||||||| || |||||||||| ||||||||||||||||
Db     397 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 456

Qy     334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG 393
           |||||||||| ||| |||| ||| ||||| |||| || |||||||||| ||||||
Db     457 CCATCTCTGACCTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCC 516

Qy     394 AGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATT 453
           |||||| |||||| ||| |||||||  || | || |||||||| |||   || || |  |
Db     517 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT 576

Qy     454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
           |    |||||||||||||||||||||||||||||||||||| ||||||||| | |||||||
Db     577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 636

Qy     514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db     637 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 696

Qy     574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633
           || |||||||||||||| ||| |||||||||||||||||| | ||  || |||||||
Db     697 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 756

Qy     634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA-----------CGAGGATGGAATAATT 681
           |  |  |||   |||  || || ||||||||           | |   ||||| ||||
Db     757 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 816

Qy     682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741
           |||| ||| ||| ||    ||| ||||||||||||||||||||||  ||||||||||||
Db     817 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCT 876

Qy     742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG 801
           ||||||||||||||| ||||| |||||||||||||||| ||||||||||||| ||||
Db     877 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 936

Qy     802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA 861
           | |||||  | |||||||||||||||||||| |||||||||| ||||||| ||||
Db     937 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 996

Qy     862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921
           ||||| |||||||||||||||||||||||||||| ||||||| ||| ||    ||| | |
Db     997 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA 1056

Qy     922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA 981
           |||||||||| | |||||||||||||||||||||||||| ||||||||||||
Db    1057 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 1116

Qy     982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC 1041
           | |||||||||||||||| || ||||||||||||||  || ||||  || |||||||
Db    1117 ACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 1176

Qy    1042 GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 1101
           |||||||||  |||| ||||||||||||   ||| |  ||||| |    ||| |   |
Db    1177 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCG 1236

Qy    1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTAT 1161
           |  |||  |  |||    |||| |  |||||||||||||||||| | || |  || || |
Db    1237 AGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT 1296

Qy    1162 AAAACGAGGAGCAGTTTGATTGT 1184
           | |||      |||  | | ||
Db    1297 GACACGGACTCAAGTGGGCTGGT 1319


RESULT 10
US-09-939-226-2
; Sequence 2, Application US/09939226
; Patent No. US20020110805A1
;   GENERAL INFORMATION:
;       APPLICANT: SAMSON, MICHEL
;                  PARMENTIER, MARC
;                  VASSART, GILBERT
;                  LIBERT, FREDERICK
;       TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                           AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;       NUMBER OF SEQUENCES: 17
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive  16th Floor
;            CITY: Newport Beach
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 92660
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/939,226
;            FILING DATE: 24-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/626,939
;            FILING DATE: 2000-07-27
;       ATTORNEY/AGENT INFORMATION:
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```
;            NAME: Altman, Daniel E
;            REGISTRATION NUMBER: 34,115
;            REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 1477 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  240..1295
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-939-226-2

  Query Match             35.5%;  Score 703.4;  DB 10;  Length 1477;
  Best Local Similarity   80.5%;  Pred. No. 3.1e-201;
  Matches  840;  Conservative    0;  Mismatches  191;  Indels   12;  Gaps    1;

Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213
          ||||| ||      |  ||||| || ||| |  | ||||||||||| |  ||||  ||||
Db    277 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 336

Qy    214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCC 273
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| |||
Db    337 TGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCC 396

Qy    274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333
          ||||| | |||||||||||| ||||||| || |||||||||| ||||||||||||||||
Db    397 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 456

Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG 393
          |||||||||| ||| |||| ||| ||||| |||| || ||||||||| ||||||
Db    457 CCATCTCTGACCTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCC 516

Qy    394 AGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATT 453
          |||||| |||||| ||| |||||||  || | || |||||||| |||   || || |  |
Db    517 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT 576

Qy    454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513
          |    |||||||||||||||||||||||||||||||| ||||||||| | |||||||
Db    577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 636

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db    637 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 696

Qy    574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633
          || |||||||||||||||| ||| |||||||||||||||| | ||  || |||||||
Db    697 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 756

Qy    634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA-----------CGAGGATGGAATAATT 681
           |  |  |||   |||  || || ||||||||           | |   ||||| ||||
Db    757 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 816

Qy    682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741
          |||| ||| ||| ||    ||| |||||||||||||||||||||  ||||||||||||
Db    817 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCT 876

Qy    742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG 801
          |||||||||||||||| ||||| |||||||||||||||| ||||||||||||||| ||||
Db    877 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 936

Qy    802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA 861
          | |||||  | |||||||||||||||||||||||| |||||||||||| ||||||| ||||
Db    937 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 996

Qy    862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921
          ||||| |||||||||||||||||||||||||| ||||||| ||| ||    ||| | |
Db    997 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA 1056

Qy    922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA 981
          |||||||||| | |||||||||||||||||||||||||| ||||||||||||
Db   1057 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 1116

Qy    982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC 1041
          | |||||||||||||||| || ||||||||||||||||  || ||||  || |||||||
Db   1117 ACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 1176

Qy   1042 GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 1101
           |||||||||  |||| ||||||||||||   ||| |  ||||| |    ||| |    |
Db   1177 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCG 1236

Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTAT 1161
          |  |||  |  |||    |||| |  ||||||||||||||||| | || |  || || |
Db   1237 AGCGAGCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTTGT 1296

Qy   1162 AAAACGAGGAGCAGTTTGATTGT 1184
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Db   1297 GACACGGACTCAAGTGGGCTGGT 1319


RESULT 11
US-09-938-703-2
; Sequence 2, Application US/09938703
; Patent No. US20020110870A1
;   GENERAL INFORMATION:
;        APPLICANT: SAMSON, MICHEL
;                   PARMENTIER, MARC
;                   VASSART, GILBERT
;                   LIBERT, FREDERICK
;        TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
;                            AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Knobbe, Martens, Olson & Bear
;            STREET: 620 Newport Center Drive  16th Floor
;            CITY: Newport Beach
;            STATE: CA
;            COUNTRY: U.S.A.
;            ZIP: 92660
;        COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/938,703
;            FILING DATE: 24-Aug-2001
;            CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/626,939
;            FILING DATE: 2000-07-27
;        ATTORNEY/AGENT INFORMATION:
;            NAME: Altman, Daniel E
;            REGISTRATION NUMBER: 34,115
;            REFERENCE/DOCKET NUMBER: <Unknown>
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 1477 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  240..1295
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-938-703-2

  Query Match             35.5%;  Score 703.4;  DB 10;  Length 1477;
  Best Local Similarity   80.5%;  Pred. No. 3.1e-201;
  Matches  840;  Conservative    0;  Mismatches  191;  Indels   12;  Gaps    1;

Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213
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Db    277 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 336

Qy    214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCC 273

Db    337 TGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCC 396

Qy    274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333

Db    397 TCATCCTGATAAACTGCAAAAGGCTGAAGAGCATGACTGACATCTACCTGCTCAACCTGG 456

Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG 393

Db    457 CCATCTCTGACCTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCC 516

Qy    394 AGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATT 453

Db    517 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT 576

Qy    454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513

Db    577 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 636

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573

Db    637 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 696

Qy    574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633

Db    697 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 756

Qy    634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA----------CGAGGATGGAATAATT 681

Db    757 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 816

Qy    682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741

Db    817 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCT 876

Qy    742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG 801

Db    877 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 936

Qy    802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA 861

Db    937 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 996

Qy    862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921

Db    997 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA 1056

Qy    922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA 981

Db   1057 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 1116

Qy    982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC 1041

Db   1117 ACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 1176

Qy   1042 GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 1101

Db   1177 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCG 1236

Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTAT 1161

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Qy   1162 AAAACGAGGAGCAGTTTGATTGT 1184

Db   1297 GACACGGACTCAAGTGGGCTGGT 1319


RESULT 12
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US-09-734-221A-13
; Sequence 13, Application US/09734221A
; Publication No. US20030096221A1
;   GENERAL INFORMATION:
;        APPLICANT: LITTMAN, DAN R.
;                   DENG, HONGKUI
;                   ELLMEIER, WILFRIED
;                   LANDAU, NATHANIEL R.
;                   LIU, RONG
;        TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
;                            MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
;                            USES THEREOF
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: David A. Jackson, Esq.
;             STREET: 411 Hackensack Ave, Continental Plaza, 4th
;                     Floor
;             CITY: Hackensack
;             STATE: New Jersey
;             COUNTRY: USA
;             ZIP: 07601
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/734,221A
;             FILING DATE: 11-Dec-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/666,020
;             FILING DATE: 19-JUN-1996
;             APPLICATION NUMBER: US 08/227,319
;             FILING DATE: 13-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Jackson Esq., David A.
;             REGISTRATION NUMBER: 26,742
;             REFERENCE/DOCKET NUMBER: 1049-1-004 N2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 201-487-5800
;             TELEFAX: 201-343-1684
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 3383 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        HYPOTHETICAL: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Homo sapiens
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-734-221A-13

  Query Match             35.5%;  Score 703.4;  DB 9;  Length 3383;
  Best Local Similarity   80.5%;  Pred. No. 5.6e-201;
  Matches  840;  Conservative    0;  Mismatches  191;  Indels   12;  Gaps    1;

Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213

Db     92 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 151

Qy    214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCC 273

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Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG 393
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Db    272 CCATCTCTGACCTGTTTTTCCTTCTTACTGTCCCCTTCTGGGCTCACTATGCTGCCGCCC 331

Qy    394 AGTGGGTCTTTGGGAATGCAATGTGCAAATTATTCACAGGGCTGTATCACATCGGTTATT 453

Db    332 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT 391

Qy    454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513

Db    392 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 451

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573

Db    452 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 511

Qy    574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633

Db    512 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 571

Qy    634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA----------CGAGGATGGAATAATT 681

Db    572 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 631

Qy    682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741

Db    632 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCT 691

Qy    742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG 801

Db    692 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 751

Qy    802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA 861

Db    752 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 811

Qy    862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921

Db    812 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA 871

Qy    922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA 981

Db    872 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 931

Qy    982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC 1041

Db    932 ACCCCATCATCTATGCCTTTGTCGGGGAGAAGTTCAGAAACTACCTCTTAGTCTTCTTCC 991

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Db   1112 GACACGGACTCAAGTGGGCTGGT 1134


RESULT 13
US-10-106-623-1
; Sequence 1, Application US/10106623
; Patent No. US20020150888A1
;   GENERAL INFORMATION:
;        APPLICANT: Gray, Patrick W.
;                   Schweickart, Vicky L.
;                   Raport, Carol J.
;        TITLE OF INVENTION: Chemokine Receptor Materials and Methods
;        NUMBER OF SEQUENCES: 20
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;             STREET: 6300 Sears Tower, 233 S. Wacker Drive
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/106,623
;             FILING DATE: 26-Mar-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/771,276
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: No. US20020150888A1and, Greta E.
;             REGISTRATION NUMBER: 35,302
;             REFERENCE/DOCKET NUMBER: 27866/33670
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 312-474-6300
;             TELEFAX: 312-474-0448
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 3383 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  55..1110
;        FEATURE:
;             NAME/KEY:  misc_feature
;             OTHER INFORMATION:  /= "88C polynucleotide and amino acid
;             sequences"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-106-623-1

  Query Match             35.5%;  Score 703.4;  DB 12;  Length 3383;
  Best Local Similarity   80.5%;  Pred. No. 5.6e-201;
  Matches  840;  Conservative    0;  Mismatches  191;  Indels   12;  Gaps    1;

Qy    154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213

Db     92 ATTATTATACATCGGAGCCCTGCCAAAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCC 151

Qy    214 TGCCTCCGCTCTACTCGCTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCGTCC 273

Db    152 TGCCTCCGCTCTACTCACTGGTGTTCATCTTTGGTTTTGTGGGCAACATGCTGGTCATCC 211

Qy    274 TCATCTTAATAAACTGCAAAAAGCTGAAGTGCTTGACTGACATTTACCTGCTCAACCTGG 333

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Qy    334 CCATCTCTGATCTGCTTTTTCTTATTACTCTCCCATTGTGGGCTCACTCTGCTGCAAATG 393

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Db    332 AGTGGGACTTTGGAAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCT 391

Qy    454 TTGGCGGAATCTTCTTCATCATCCTCCTGACAATCGATAGATACCTGGCTATTGTCCATG 513

Db    392 TCTCTGGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTGTCGTCCATG 451

Qy    514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573

Db    452 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTT 511

Qy    574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633

Db    512 GGGTGGTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAG 571

Qy    634 ATTCTGTTTATGTCTGTGGCCCTTATTTTCCA----------CGAGGATGGAATAATT 681

Db    572 GTCTTCATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATT 631

Qy    682 TCCACACAATAATGAGGAACATTTTGGGGCTGGTCCTGCCGCTGCTCATCATGGTCATCT 741

Db    632 TCCAGACATTAAAGATAGTCATCTTGGGGCTGGTCCTGCCGCTGCTTGTCATGGTCATCT 691

Qy    742 GCTACTCGGGAATCCTGAAAACCCTGCTTCGGTGTCGAAACGAGAAGAAGAGGCATAGGG 801

Db    692 GCTACTCGGGAATCCTAAAAACTCTGCTTCGGTGTCGAAATGAGAAGAAGAGGCACAGGG 751

Qy    802 CAGTGAGAGTCATCTTCACCATCATGATTGTTTACTTTCTCTTCTGGACTCCCTATAACA 861

Db    752 CTGTGAGGCTTATCTTCACCATCATGATTGTTTATTTTCTCTTCTGGGCTCCCTACAACA 811

Qy    862 TTGTCATTCTCCTGAACACCTTCCAGGAATTCTTCGGCCTGAGTAACTGTGAAAGCACCA 921

Db    812 TTGTCCTTCTCCTGAACACCTTCCAGGAATTCTTTGGCCTGAATAATTGCAGTAGCTCTA 871

Qy    922 GTCAACTGGACCAAGCCACGCAGGTGACAGAGACTCTTGGGATGACTCACTGCTGCATCA 981

Db    872 ACAGGTTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCA 931

Qy    982 ATCCCATCATCTATGCCTTCGTTGGGGAGAAGTTCAGAAGGTATCTCTCGGTGTTCTTCC 1041

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Qy   1042 GAAAGCACATCACCAAGCGCTTCTGCAAACAATGTCCAGTTTTCTACAGGGAGACAGTGG 1101

Db    992 AAAAGCACATTGCCAAACGCTTCTGCAAATGCTGTTCTATTTTCCAGCAAGAGGCTCCCG 1051

Qy   1102 ATGGAGTGACTTCAACAAACACGCCTTCCACTGGGGAGCAGGAAGTCTCGGCTGGTTTAT 1161

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Qy   1162 AAAACGAGGAGCAGTTTGATTGT 1184

Db   1112 GACACGGACTCAAGTGGGCTGGT 1134
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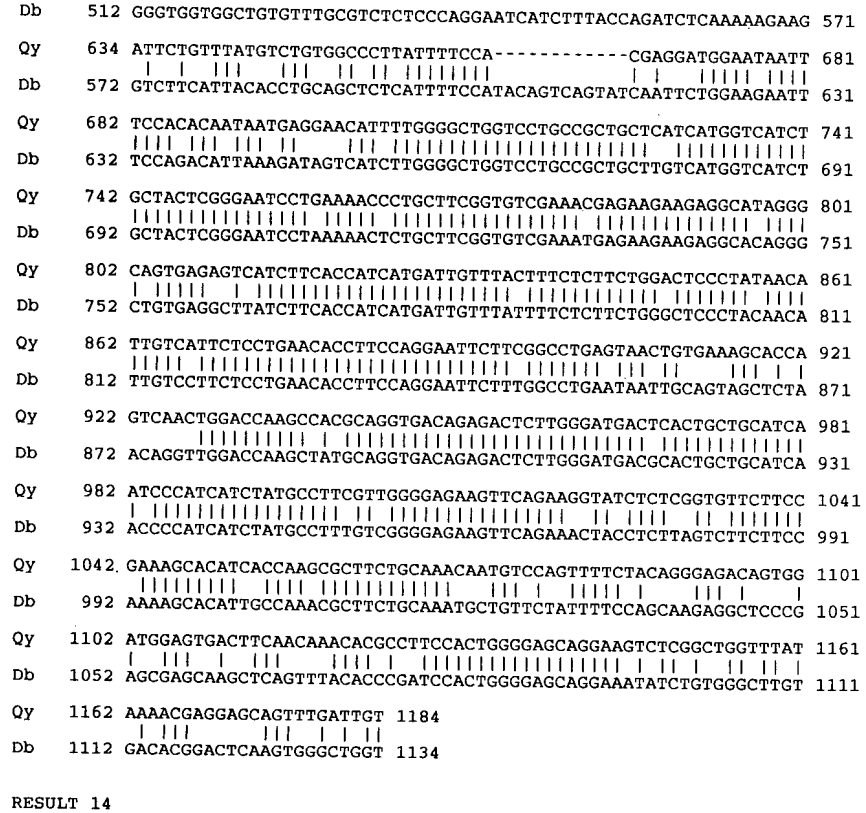
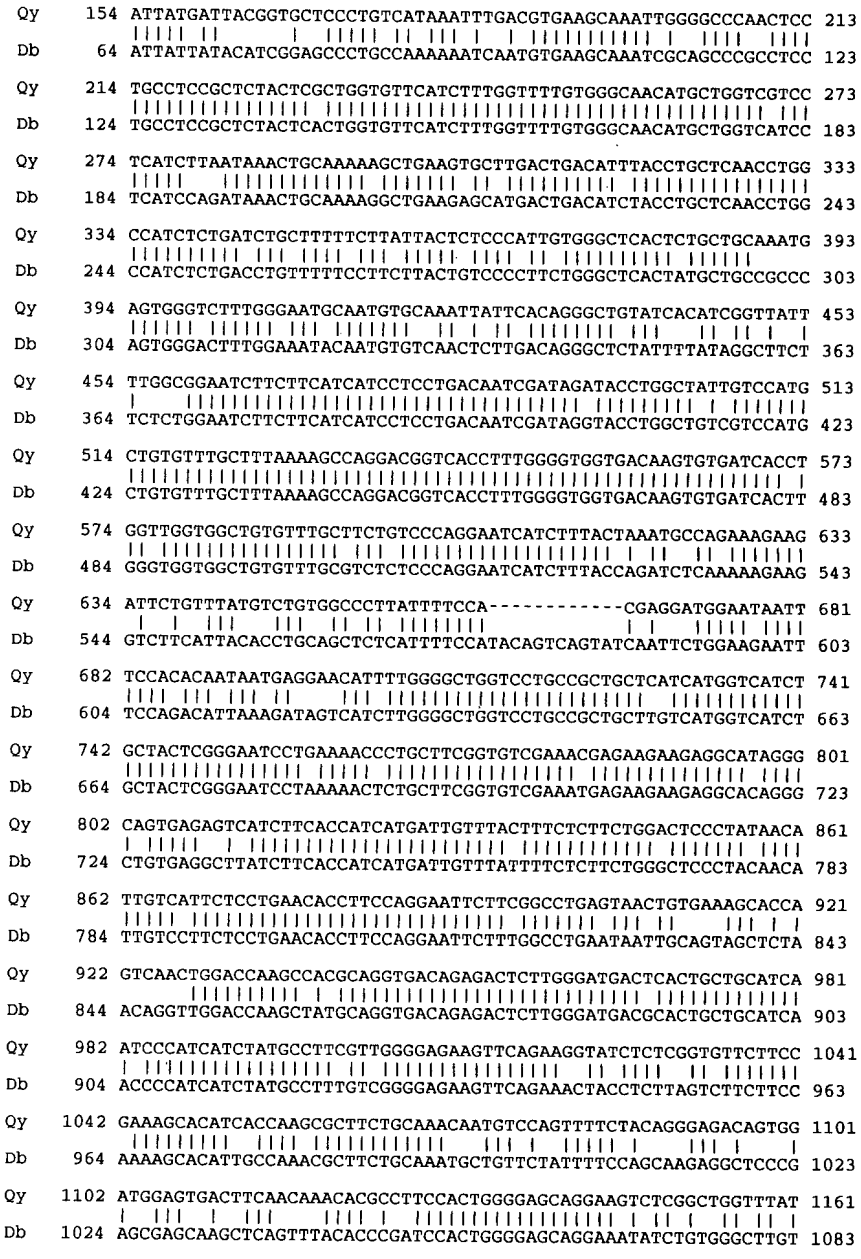


RESULT 14
US-09-813-653-16
; Sequence 16, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(1085)
US-09-813-653-16

Query Match 35.5%; Score 701.8; DB 10; Length 1225;
Best Local Similarity 80.4%; Pred. No. 8.4e-201;
Matches 839; Conservative 0; Mismatches 192; Indels 12; Gaps 1;



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Db   1084 GACACGGACTCAAGTGGGCTGGT 1106


RESULT 15
US-10-232-686-1
; Sequence 1, Application US/10232686
; Publication No. US20030023044A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Yi
;  APPLICANT:  Ruben, Steven M.
;  TITLE OF INVENTION: Human G-Protein Chemokine Receptor (CCR5) HDGNR10
;  FILE REFERENCE: 1488.115000N
;  CURRENT APPLICATION NUMBER: US/10/232,686
;  CURRENT FILING DATE:  2002-09-03
;  PRIOR APPLICATION NUMBER: 09/339,912
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 09/195,662
;  PRIOR FILING DATE: 1998-11-18
;  PRIOR APPLICATION NUMBER: 08/466,343
;  PRIOR FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1414
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (259)..(1314)
US-10-232-686-1

  Query Match             35.5%;  Score 701.8;  DB 9;  Length 1414;
  Best Local Similarity   80.4%;  Pred. No. 9.3e-201;
  Matches  839;  Conservative    0;  Mismatches  192;  Indels   12;  Gaps    1;

Qy     154 ATTATGATTACGGTGCTCCCTGTCATAAATTTGACGTGAAGCAAATTGGGGCCCAACTCC 213
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           |    |||||||||||||||||||||||||||||||||||||| ||||||||| | |||||||
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Qy     514 CTGTGTTTGCTTTAAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACCT 573
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
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Qy     574 GGTTGGTGGCTGTGTTTGCTTCTGTCCCAGGAATCATCTTTACTAAATGCCAGAAAGAAG 633
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Search completed: June  1, 2003, 20:21:15
Job time : 385.669 secs
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